



1/26

SEQUENCE LISTING

<110> Abbott Laboratories
Mukerji, Pradip
Huang, Yung-Sheng
Pereira, Suzette L.

<120> DESATURASE GENES, ENZYMES ENCODED
THEREBY, AND USES THEREOF

<130> 6884.US.O1

<140> 10/060,793

<141> 2002-01-30

<160> 60

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<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

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<400> 1

atccgcgccg ccatecccaa gcactgctgg gtcaag

36

<210> 2

<211> 45

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<213> Artificial Sequence

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<221> misc_feature

<222> (21)...(21)

<223> y = t/u or c at position 21

<221> misc_feature

<222> (33)...(33)

<223> y = t/u or c at position 33

<400> 2

gccctcttcg tcctcgcca ygactgcggc cayggctcgt tctcg

45

<210> 3

<211> 45

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<213> Artificial Sequence

<220>

<223> Reverse Primer RO1118

<221> misc_feature

<222> (4)...(4)

<223> r = g or a at position 4

<221> misc_feature

<222> (10)...(10)

<223> r = g or a at position 10

<221> misc_feature

<222> (30)...(31)

<223> r = g or a at positions 30-31

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<222> (39)...(39)

<223> y = t/u or c at position 39

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<222> (43)...(43)

<223> r = g or a at position 43

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gagrtggtar tgggggatct gggggaagar rtgrtggrtg acrtg

45

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<221> misc_feature

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<223> y = t/u or c at position 9

<221> misc_feature

<222> (27)...(27)

<223> y = t/u or c at position 27

<221> misc_feature

<222> (36)...(36)

<223> y = t/u or c at position 36

<221> misc_feature

<222> (39)...(39)

<223> y = t/u or c at position 39

<400> 4

ccctaccayg gctggcgcat ctcgcaycgc acccaycayc agaac

45

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> r = g or a at position 7

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (37)...(37)
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<222> (13)...(13)
<223> s = g or c at position 13

<221> misc_feature
<222> (19)...(19)
<223> k = g or t/u at position 19

<400> 6
ggctcgcaact tcsaccccka ctcggacctc ttcgtc
36

<210> 7
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<223> m = a or c at position 18

<221> misc_feature
<222> (24)...(24)
<223> w = a or t/u at position 24

<400> 7
gacgaagagg tccgagtmgg ggtwgaagtg cgagcc
36

<210> 8
<211> 39
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<213> Artificial Sequence

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<223> Reverse Primer RO1148

<221> misc_feature

<222> (9)...(9)

<223> k = g or t/u at position 9

<221> misc_feature

<222> (30)...(30)

<223> w = a or t/u at position 30

<221> misc_feature

<222> (32)...(32)

<223> s = g or c at position 32

<400> 8

gcgctggakg gtggtgaggc cgccgcggaw gsacgacca

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<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Reverse Primer RO1114

<221> misc_feature

<222> (13)...(13)

<223> r = g or a at position 13

<221> misc_feature

<222> (16)...(16)

<223> r = g or a at position 16

<221> misc_feature

<222> (25)...(25)

<223> r = g or a at position 25

<221> misc_feature

<222> (40)...(40)

<223> r = g or a at position 40

<221> misc_feature

<222> (43)...(43)

<223> r = g or a at position 43

<400> 9

ctgggggaag agrtgrtgga tgacrtgggt gccgatgtcr tgrtg

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<210> 10

<211> 45

<212> DNA

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<220>

<223> Reverse Primer RO1116

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<221> misc_feature
 <222> (16)...(16)
 <223> r = g or a at position 16

<221> misc_feature
 <222> (22)...(22)
 <223> r = g or a at position 22

<221> misc_feature
 <222> (33)...(33)
 <223> k = g or t/u at position 33

<221> misc_feature
 <222> (42)...(43)
 <223> r = g or at at positions 42-43

<400> 10
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45

<210> 11
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 <223> Reverse Primer R01118

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<221> misc_feature
 <222> (10)...(10)
 <223> r = g or a at position 10

<221> misc_feature
 <222> (30)...(31)
 <223> r = g or a at positions 30-31

<221> misc_feature
 <222> (34)...(34)
 <223> r = g or a at position 34

<221> misc_feature
 <222> (38)...(38)
 <223> r = g or a at position 38

<221> misc_feature
 <222> (39)...(39)
 <223> y = t/u or c at position 39

<221> misc_feature
 <222> (43)...(43)
 <223> r = g or a at position 43

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45

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 <210> 13
 <211> 27
 <212> DNA
 <213> Artificial Sequence

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 <223> Forward Primer RO1189

 <400> 13
 ttcttgcacc acaacgacga agcgacg 27

 <210> 14
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 <212> DNA
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 <400> 14
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 <210> 15
 <211> 26
 <212> DNA
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 <220>
 <223> Forward Primer RO1191

 <400> 15
 tcaagggcaa cctctcgagc gtcgac 26

 <210> 16
 <211> 31
 <212> DNA
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 <220>
 <223> Primer RO898

 <400> 16
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 <210> 17
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 <212> DNA
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 <213> Artificial Sequence

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 <223> Reverse Primer RO1185

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 <210> 19
 <211> 20
 <212> DNA
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 <223> Reverse Primer RO1186

 <400> 19
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 <210> 20
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 <210> 22
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 <400> 22

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<210> 23

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Forward Primer RO1221

<400> 23

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<210> 24

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse Primer RO1222

<400> 24

aaaagagaat tccgcttcct agtcttagtc cgacttggcc ttggc 45

<210> 25

<211> 1077

<212> DNA

<213> Saprolegnia diclina

<400> 25

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ttcaacgcgt	cggcctcggc	ggcgctgctc	tacgcggcgc	gctcgacgcc	gttcattgcc	180
gataacgttc	tgctccacgc	gctcggtttg	gccacctaca	tctacgtgca	gggcgtcatc	240
ttctggggct	tcttcacggt	cggccacgac	tgcggccact	cggccttctc	gcgctaccac	300
agcgtcaact	ttatcatcgg	ctgcatcatg	cactctgcga	ttttgacgcc	gttcgagagc	360
tggcgcgtga	cgcaccgcca	ccaccacaag	aacacgggca	acattgataa	ggacgagatc	420
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ggcgggtgct	ggtttgtcta	cttgaaggtc	gggtatgccc	cgcgcacgat	gagccacttt	540
gacccgtggg	accgcgtcct	ccttcgcgcg	gcgtcggccg	tcctcgtgct	gctcggcgct	600
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ttgcaccaca	acgacgaagc	gacgcgcgtg	tacggcgact	cggagtggac	gtacgtcaag	780
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gccaccaagc	actttgcggc	cgcgtacccg	cacctcgtgc	gcaggaacga	cgagcccatc	960
atcacggcct	tcttcaagac	cgcgcacctc	tttgtcaact	acggcgctgt	gcccagagacg	1020
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<210> 26

<211> 358

<212> PRT

<213> Saprolegnia diclina

<400> 26

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			20					25					30		
Leu	Tyr	Tyr	Thr	Ala	Arg	Ala	Ile	Phe	Asn	Ala	Ser	Ala	Ser	Ala	Ala

	35		40		45										
Leu	Leu	Tyr	Ala	Ala	Arg	Ser	Thr	Pro	Phe	Ile	Ala	Asp	Asn	Val	Leu
	50					55					60				
Leu	His	Ala	Leu	Val	Cys	Ala	Thr	Tyr	Ile	Tyr	Val	Gln	Gly	Val	Ile
65					70					75					80
Phe	Trp	Gly	Phe	Phe	Thr	Val	Gly	His	Asp	Cys	Gly	His	Ser	Ala	Phe
				85					90					95	
Ser	Arg	Tyr	His	Ser	Val	Asn	Phe	Ile	Ile	Gly	Cys	Ile	Met	His	Ser
			100					105					110		
Ala	Ile	Leu	Thr	Pro	Phe	Glu	Ser	Trp	Arg	Val	Thr	His	Arg	His	His
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His	Lys	Asn	Thr	Gly	Asn	Ile	Asp	Lys	Asp	Glu	Ile	Phe	Tyr	Pro	His
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Arg	Ser	Val	Lys	Asp	Leu	Gln	Asp	Val	Arg	Gln	Trp	Val	Tyr	Thr	Leu
145					150					155					160
Gly	Gly	Ala	Trp	Phe	Val	Tyr	Leu	Lys	Val	Gly	Tyr	Ala	Pro	Arg	Thr
				165					170					175	
Met	Ser	His	Phe	Asp	Pro	Trp	Asp	Pro	Leu	Leu	Leu	Arg	Arg	Ala	Ser
			180					185					190		
Ala	Val	Ile	Val	Ser	Leu	Gly	Val	Trp	Ala	Ala	Phe	Phe	Ala	Ala	Tyr
		195					200					205			
Ala	Tyr	Leu	Thr	Tyr	Ser	Leu	Gly	Phe	Ala	Val	Met	Gly	Leu	Tyr	Tyr
	210					215					220				
Tyr	Ala	Pro	Leu	Phe	Val	Phe	Ala	Ser	Phe	Leu	Val	Ile	Thr	Thr	Phe
225					230					235					240
Leu	His	His	Asn	Asp	Glu	Ala	Thr	Pro	Trp	Tyr	Gly	Asp	Ser	Glu	Trp
			245						250					255	
Thr	Tyr	Val	Lys	Gly	Asn	Leu	Ser	Ser	Val	Asp	Arg	Ser	Tyr	Gly	Ala
		260						265					270		
Phe	Val	Asp	Asn	Leu	Ser	His	His	Ile	Gly	Thr	His	Gln	Val	His	His
		275					280					285			
Leu	Phe	Pro	Ile	Ile	Pro	His	Tyr	Lys	Leu	Asn	Glu	Ala	Thr	Lys	His
	290					295					300				
Phe	Ala	Ala	Ala	Tyr	Pro	His	Leu	Val	Arg	Arg	Asn	Asp	Glu	Pro	Ile
305					310					315					320
Ile	Thr	Ala	Phe	Phe	Lys	Thr	Ala	His	Leu	Phe	Val	Asn	Tyr	Gly	Ala
			325						330					335	
Val	Pro	Glu	Thr	Ala	Gln	Ile	Phe	Thr	Leu	Lys	Glu	Ser	Ala	Ala	Ala
		340						345					350		
Ala	Lys	Ala	Lys	Ser	Asp										
		355													

<210> 27

<211> 1413

<212> DNA

<213> Saprolegnia diclina

<400> 27

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atcattatcc	gcggcaaggt	ctacgacgtg	accgagtggg	ccaacaagca	ccccggcggc	180
cgcgagatgg	tgctgctgca	cgccggtcgc	gaggccaccg	acacgttcga	ctcgtagcac	240
ccgttcagcg	acaaggccga	gtcgatcttg	aacaagtatg	agattggcac	gttcacgggc	300
ccgtccgagt	ttccgacctt	caagccggac	acgggcttct	acaaggagtg	ccgcaagcgc	360
gttggcgagt	acttcaagaa	gaacaacctc	catccgcagg	acggcttccc	gggcctctgg	420
cgcgatgatg	tcgtgtttgc	ggtcgccggc	ctcgctttgt	acggcatgca	cttttcgact	480
atctttgcgc	tgcagctcgc	ggccgcggcg	ctctttggcg	tctgccaggc	gctgccgctg	540
ctccacgtca	tgcacgactc	gtcgcacgcg	tcgtacacca	acatgccgtt	cttcattac	600
gtcgtcggcc	gctttgccat	ggactggttt	gccggcggtc	cgatgggtgc	atggctcaac	660
cagcacgtcg	tgggcccacca	catctacacg	aacgtcgcgc	gctcggaccc	ggatcttccg	720

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gtcaacatgg acggcgacat ccgcccgcac gtgaaccgcc aggtgttcca gcccatgtac      780
gcattccagc acatctacct tccgcccgtc tatggcgtgc ttggcctcaa gttccgcac      840
caggacttca ccgacacgtt cggtcgcac acgaacggcc cgatccgcgt caaccgcac      900
gcgctctcga cgtggatggc catgatcagc tccaagtcgt tctgggcctt ctaccgcgtg      960
taccttccgc ttgccgtgct ccagatgcc atcaagacgt acctgcgat cttcttctc      1020
gccgagtttg tcacgggctg gtacctcgcg ttcaacttcc aagtaagcca tgtctcgacc      1080
gagtgcggct acccatgcgg cgacgaggcc aagatggcgc tccaggacga gtgggcagtc      1140
tcgcaggtca agacgtcggg cgactacgcc catggctcgt ggatgacgac gttccttgcc      1200
ggcgcgctca actaccaggt cgtgcaccac ttgttcccca gcgtgtcgca gtaccactac      1260
ccggcgatcg cgcccatcat cgtcgacgtc tgcaaggagt acaacatcaa gtacgccatc      1320
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cagggcatcg ccgccacgat ccacatgggc taa                                1413

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<210> 28

<211> 819

<212> DNA

<213> Thraustochytrid sp.

<400> 28

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tggatggatg gcgccaagcc gtacgcactc accgatgggc tcccgatgat ggacgtgtcc      120
accatgctgg cattcgaggt gggatacatg gccatgctgc tcttcggcat cccgatcatg      180
aagcagatgg agaagccttt tgagctcaag accatcaagc tcttgacaaa cttgtttctc      240
ttcggacttt ccttgtacat gtgcgtggag accatccgcc aggctatcct cggaggctac      300
aaagtgtttg gaaacgacat ggagaaggcc aacgagtctc atgctcaggg catgtctcgc      360
atcgtgtacg tgttctgcgt gtccaaggca tacgagttct tggataccgc catcatgac      420
ctttgcaaga agttcaacca ggtttccttc ttgcatgtgt accaccatgc caccattttt      480
gccatctggt gggctatcgc caagtacgct ccaggaggtg atgctactt ttcagtgatc      540
ctcaactctt tcgtgcacac cgatcatgtac gcatactact tcttctcctc ccaagggttc      600
gggttcgtga agccaatcaa gccgtacatc accacccttc agatgaccca gttcatggca      660
atgcttgtgc agtccttgta cgactacctc ttcccatgcg actaccaca ggctcttggtg      720
cagcttcttg gagtgtacat gatcaccttg cttgccctct tcggcaactt ttttgtgcag      780
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<210> 29

<211> 515

<212> PRT

<213> Saprolegnia diclina

<400> 29

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Met Thr Val Gly Phe Asp Glu Thr Val Thr Met Asp Thr Val Arg Asn
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His Asn Met Pro Asp Asp Ala Trp Cys Ala Ile His Gly Thr Val Tyr
      20          25          30
Asp Ile Thr Lys Phe Ser Lys Val His Pro Gly Gly Asp Ile Ile Met
      35          40          45
Leu Ala Ala Gly Lys Glu Ala Thr Ile Leu Phe Glu Thr Tyr His Ile
      50          55          60
Lys Gly Val Pro Asp Ala Val Leu Arg Lys Tyr Lys Val Gly Lys Leu
      65          70          75          80
Pro Gln Gly Lys Lys Gly Glu Thr Ser His Met Pro Thr Gly Leu Asp
      85          90          95
Ser Ala Ser Tyr Tyr Ser Trp Asp Ser Glu Phe Tyr Arg Val Leu Arg
      100         105         110
Glu Arg Val Ala Lys Lys Leu Ala Glu Pro Gly Leu Met Gln Arg Ala
      115         120         125
Arg Met Glu Leu Trp Ala Lys Ala Ile Phe Leu Leu Ala Gly Phe Trp
      130         135         140
Gly Ser Leu Tyr Ala Met Cys Val Leu Asp Pro His Gly Gly Ala Met
      145         150         155         160

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Val	Ala	Ala	Val	Thr	Leu	Gly	Val	Phe	Ala	Ala	Phe	Val	Gly	Thr	Cys
				165					170					175	
Ile	Gln	His	Asp	Gly	Ser	His	Gly	Ala	Phe	Ser	Lys	Ser	Arg	Phe	Met
			180					185					190		
Asn	Lys	Ala	Ala	Gly	Trp	Thr	Leu	Asp	Met	Ile	Gly	Ala	Ser	Ala	Met
		195					200					205			
Thr	Trp	Glu	Met	Gln	His	Val	Leu	Gly	His	His	Pro	Tyr	Thr	Asn	Leu
	210					215					220				
Ile	Glu	Met	Glu	Asn	Gly	Leu	Ala	Lys	Val	Lys	Gly	Ala	Asp	Val	Asp
225					230					235					240
Pro	Lys	Lys	Val	Asp	Gln	Glu	Ser	Asp	Pro	Asp	Val	Phe	Ser	Thr	Tyr
			245					250						255	
Pro	Met	Leu	Arg	Leu	His	Pro	Trp	His	Arg	Gln	Arg	Phe	Tyr	His	Lys
			260					265					270		
Phe	Gln	His	Leu	Tyr	Ala	Pro	Leu	Ile	Phe	Gly	Phe	Met	Thr	Ile	Asn
		275					280					285			
Lys	Val	Ile	Ser	Gln	Asp	Val	Gly	Val	Val	Leu	Arg	Lys	Arg	Leu	Phe
	290					295					300				
Gln	Ile	Asp	Ala	Asn	Cys	Arg	Tyr	Gly	Ser	Pro	Trp	Asn	Val	Ala	Arg
305					310					315					320
Phe	Trp	Ile	Met	Lys	Leu	Leu	Thr	Thr	Leu	Tyr	Met	Val	Ala	Leu	Pro
			325						330					335	
Met	Tyr	Met	Gln	Gly	Pro	Ala	Gln	Gly	Leu	Lys	Leu	Phe	Phe	Met	Ala
			340					345					350		
His	Phe	Thr	Cys	Gly	Glu	Val	Leu	Ala	Thr	Met	Phe	Ile	Val	Asn	His
		355					360					365			
Ile	Ile	Glu	Gly	Val	Ser	Tyr	Ala	Ser	Lys	Asp	Ala	Val	Lys	Gly	Val
	370					375					380				
Met	Ala	Pro	Pro	Arg	Thr	Val	His	Gly	Val	Thr	Pro	Met	Gln	Val	Thr
385					390					395					400
Gln	Lys	Ala	Leu	Ser	Ala	Ala	Glu	Ser	Thr	Lys	Ser	Asp	Ala	Asp	Lys
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Thr	Thr	Met	Ile	Pro	Leu	Asn	Asp	Trp	Ala	Ala	Val	Gln	Cys	Gln	Thr
		420						425					430		
Ser	Val	Asn	Trp	Ala	Val	Gly	Ser	Trp	Phe	Trp	Asn	His	Phe	Ser	Gly
		435					440					445			
Gly	Leu	Asn	His	Gln	Ile	Glu	His	His	Cys	Phe	Pro	Gln	Asn	Pro	His
	450					455					460				
Thr	Val	Asn	Val	Tyr	Ile	Ser	Gly	Ile	Val	Lys	Glu	Thr	Cys	Glu	Glu
465					470					475					480
Tyr	Gly	Val	Pro	Tyr	Gln	Ala	Glu	Ile	Ser	Leu	Phe	Ser	Ala	Tyr	Phe
			485						490					495	
Lys	Met	Leu	Ser	His	Leu	Arg	Thr	Leu	Gly	Asn	Glu	Asp	Leu	Thr	Ala
			500					505					510		
Trp	Ser	Thr													
		515													

<210> 30

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward Primer R0967

<221> misc_feature

<222> (4)...(4)

<223> s = g or c at position 4

<221> misc_feature

<222> (12)...(12)
 <223> s = g or c at position 12

<221> misc_feature
 <222> (30)...(30)
 <223> s = g or c at position 30

<221> misc_feature
 <222> (31)...(31)
 <223> k = g or t/u at position 31

<221> misc_feature
 <222> (32)...(32)
 <223> s = g or c at position 32

<400> 30
 ccgsagttca csatcaagga gatccgcgas kscatcccg cccactgctt c

51

<210> 31
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse Primer R0968

<221> misc_feature
 <222> (2)...(2)
 <223> r = g or a at position 2

<221> misc_feature
 <222> (3)...(3)
 <223> s = g or c at position 3

<221> misc_feature
 <222> (12)...(12)
 <223> k = g or t/u at position 12

<221> misc_feature
 <222> (17)...(17)
 <223> w = a or t/u at position 17

<221> misc_feature
 <222> (18)...(18)
 <223> m = a or c at position 18

<221> misc_feature
 <222> (19)...(19)
 <223> s = g or c at position 19

<221> misc_feature
 <222> (41)...(41)
 <223> w = a or t/u at position 41

<221> misc_feature
 <222> (42)...(42)
 <223> r = g or a at position 42

<400> 31
 grscttcttg akgtggwmsg tggcctcctc ggcgtggtag wrcggcat

48

<210> 32
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward Primer R0964

<221> misc_feature
 <222> (3)...(4)
 <223> s = g or c at positions 3-4

<221> misc_feature
 <222> (25)...(25)
 <223> r = g or a at position 25

<221> misc_feature
 <222> (36)...(36)
 <223> s = g or c at position 36

<400> 32
 ccsstctact gggcctgccca gggtrtcgtc ctcacsggtg tctgg

45

<210> 33
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward Primer R0965

<221> misc_feature
 <222> (3)...(4)
 <223> s = g or c at positions 3-4

<221> misc_feature
 <222> (16)...(16)
 <223> r = g or a at position 16

<221> misc_feature
 <222> (17)...(17)
 <223> y = t/u or c at position 17

<221> misc_feature
 <222> (18)...(18)
 <223> s = g or c at position 18

<221> misc_feature
 <222> (25)...(25)
 <223> r = g or a at position 25

<221> misc_feature
 <222> (31)...(31)
 <223> k = g or t/u at position 31

<221> misc_feature
 <222> (33)...(33)
 <223> y = t/u or c at position 33

<221> misc_feature
 <222> (36)...(36)
 <223> s = g or c at position 36

<400> 33
 ccsstctact ggatcrysca gggtrtcgtc kgyacsggtg tctgg

45

<210> 34
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse Primer RO966

<221> misc_feature
 <222> (19)...(19)
 <223> s = g or c at position 19

<221> misc_feature
 <222> (20)...(21)
 <223> m = a or c at positions 20-21

<221> misc_feature
 <222> (30)...(30)
 <223> r = g or a at position 30

<400> 34
 ggcgtggttag tgcggcatsm mcgagaagar gtggtgggcg acgtg

45

<210> 35
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward Primer RO975

<400> 35
 cacgtacctc cagcacacgg acacctacg

29

<210> 36
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward Primer RO976

<400> 36
 gatcgacagc gcgatccacc acattgc

27

<210> 37
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse Primer RO977

<400> 37
 caaatggttaa aagctagtgg cagcgctgc 29

<210> 38
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse Primer RO978

<400> 38
 agtacgtgcc ctggacgaac cagtagatg 29

<210> 39
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward Primer RO1051

<400> 39
 tcaacagaat tcatgtgcaa aggtcaagct ccttccaagg ccgacgtg 48

<210> 40
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse Primer RO1057

<400> 40
 aaaagaaagc ttttactttt cctcgagctt gcgcttgtaa aacacaac 48

<210> 41
 <211> 1182
 <212> DNA
 <213> *Saprolegnia diclina*

<400> 41
 atgtgcaaaag gtcaagctcc ttccaaggcc gacgtgttcc acgctgcggg gtaccgcccg 60
 gtcgcccggca cgcccagacc gctgcccgtg gagccccga cgatcacgct caaggacctg 120
 cgcgcggcga tcccggccca ctgctttgag cgcagcgtg ccactagctt ttaccatttg 180
 gccaagaacc ttgcgatctg cgccggcggtg ttgcgccgtg gcctcaagct cgcggctgcc 240
 gacttgccgc tcgcggccaa gctggtcgcg tggcccatct actggttcgt ccagggcacg 300
 tacttttacgg gcatctgggt cattgcgcac gaatgcggcc accaggcgtt ctccggcgtc 360
 gagatcctca acgacacggt cggatatcatt cttcactcgc tcctctttgt gccgtaccac 420
 agctggaaga tcacgcaccg ccgccaccac tccaacacgg gcagctgcga gaacgacgag 480
 gtgttttacgc cgacgcgcg gtcgcgtcgc gaggccaagc acgaccactc gtcctcga 540
 gagagcccgc tctacaacct gtacggcatc gtcgatgatc ttctcgtggg ctggatgccg 600
 ggctacctct tcttcaacgc gaccggcccc accaagtacg ctggcctcgc caagtgcgac 660
 ttcaaccctg acgcagcctt tttcctccca aaggagcgcc tcagcatctg gtggagcgac 720
 ctctgcttcc tcgcggcctt gtacggcttt ggctacggcg tctcgggtct cggcctctc 780
 gatgtcgccc gccactacat cgtgcggtac ctcatcttgc acgcgtacct cgtgctcatc 840
 acgtacctcc agcacacgga tacgtacgtg ccccaacttc gcggcgacga gtggaactgg 900
 ctgcgcggcg cgctctgcac cgtcgaccgc tcgttcggcg cgtggatcga cagcgcgatc 960
 caccacattg ccgacacgca cgtgacgcac cacattttct ccaagacgcc cttctaccac 1020
 gcgatcgagg cgaccgacgc catcacgccc ctccctcgga agtactacct catcgaccgc 1080

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acgccgatcc cgctggcgct ctggcgctcg ttcacgcact gcaagtacgt cgaggacgac 1140
ggcaacgttg tgttttataa gcgcaagctc gaggaaaagt aa 1182
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<210> 42
<211> 393
<212> PRT
<213> Saprolegnia diclina
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<400>	42															
Met	Cys	Lys	Gly	Gln	Ala	Pro	Ser	Lys	Ala	Asp	Val	Phe	His	Ala	Ala	
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Gly	Tyr	Arg	Pro	Val	Ala	Gly	Thr	Pro	Glu	Pro	Leu	Pro	Leu	Glu	Pro	
			20					25					30			
Pro	Thr	Ile	Thr	Leu	Lys	Asp	Leu	Arg	Ala	Ala	Ile	Pro	Ala	His	Cys	
			35				40					45				
Phe	Glu	Arg	Ser	Ala	Ala	Thr	Ser	Phe	Tyr	His	Leu	Ala	Lys	Asn	Leu	
	50					55					60					
Ala	Ile	Cys	Ala	Gly	Val	Phe	Ala	Val	Gly	Leu	Lys	Leu	Ala	Ala	Ala	
65				70					75						80	
Asp	Leu	Pro	Leu	Ala	Ala	Lys	Leu	Val	Ala	Trp	Pro	Ile	Tyr	Trp	Phe	
				85					90					95		
Val	Gln	Gly	Thr	Tyr	Phe	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	
			100					105					110			
Gly	His	Gln	Ala	Phe	Ser	Ala	Ser	Glu	Ile	Leu	Asn	Asp	Thr	Val	Gly	
			115				120					125				
Ile	Ile	Leu	His	Ser	Leu	Leu	Phe	Val	Pro	Tyr	His	Ser	Trp	Lys	Ile	
	130					135					140					
Thr	His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser	Cys	Glu	Asn	Asp	Glu	
145				150						155					160	
Val	Phe	Thr	Pro	Thr	Pro	Arg	Ser	Val	Val	Glu	Ala	Lys	His	Asp	His	
				165					170					175		
Ser	Leu	Leu	Glu	Ser	Pro	Leu	Tyr	Asn	Leu	Tyr	Gly	Ile	Val	Met		
			180				185					190				
Met	Leu	Leu	Val	Gly	Trp	Met	Pro	Gly	Tyr	Leu	Phe	Phe	Asn	Ala	Thr	
			195				200					205				
Gly	Pro	Thr	Lys	Tyr	Ala	Gly	Leu	Ala	Lys	Ser	His	Phe	Asn	Pro	Tyr	
	210					215					220					
Ala	Ala	Phe	Phe	Leu	Pro	Lys	Glu	Arg	Leu	Ser	Ile	Trp	Trp	Ser	Asp	
225				230					235					240		
Leu	Cys	Phe	Leu	Ala	Ala	Leu	Tyr	Gly	Phe	Gly	Tyr	Gly	Val	Ser	Val	
				245					250					255		
Phe	Gly	Leu	Leu	Asp	Val	Ala	Arg	His	Tyr	Ile	Val	Pro	Tyr	Leu	Ile	
			260					265					270			
Cys	Asn	Ala	Tyr	Leu	Val	Leu	Ile	Thr	Tyr	Leu	Gln	His	Thr	Asp	Thr	
			275				280					285				
Tyr	Val	Pro	His	Phe	Arg	Gly	Asp	Glu	Trp	Asn	Trp	Leu	Arg	Gly	Ala	
	290					295					300					
Leu	Cys	Thr	Val	Asp	Arg	Ser	Phe	Gly	Ala	Trp	Ile	Asp	Ser	Ala	Ile	
305				310						315					320	
His	His	Ile	Ala	Asp	Thr	His	Val	Thr	His	His	Ile	Phe	Ser	Lys	Thr	
				325												

<210> 43
 <211> 393
 <212> PRT
 <213> Saprolegnia diclina

<400> 43

Met	Cys	Lys	Gly	Gln	Ala	Pro	Ser	Lys	Ala	Asp	Val	Phe	His	Ala	Ala		
1				5					10					15			
Gly	Tyr	Arg	Pro	Val	Ala	Gly	Thr	Pro	Glu	Pro	Leu	Pro	Leu	Glu	Pro		
			20					25					30				
Pro	Thr	Ile	Thr	Leu	Lys	Asp	Leu	Arg	Ala	Ala	Ile	Pro	Ala	His	Cys		
		35					40					45					
Phe	Glu	Arg	Ser	Ala	Ala	Thr	Ser	Phe	Tyr	His	Leu	Ala	Lys	Asn	Leu		
	50					55					60						
Ala	Ile	Cys	Ala	Gly	Val	Phe	Ala	Val	Gly	Leu	Lys	Leu	Ala	Ala	Ala		
65				70					75						80		
Asp	Leu	Pro	Leu	Ala	Ala	Lys	Leu	Val	Ala	Trp	Pro	Ile	Tyr	Trp	Phe		
				85					90					95			
Val	Gln	Gly	Thr	Tyr	Phe	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys		
			100				105						110				
Gly	His	Gln	Ala	Phe	Ser	Ala	Ser	Glu	Ile	Leu	Asn	Asp	Thr	Val	Gly		
		115				120						125					
Ile	Ile	Leu	His	Ser	Leu	Leu	Phe	Val	Pro	Tyr	His	Ser	Trp	Lys	Ile		
	130					135						140					
Thr	His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser	Cys	Glu	Asn	Asp	Glu		
145					150					155					160		
Val	Phe	Thr	Pro	Thr	Pro	Arg	Ser	Val	Val	Glu	Ala	Lys	His	Asp	His		
				165					170					175			
Ser	Leu	Leu	Glu	Glu	Ser	Pro	Leu	Tyr	Asn	Leu	Tyr	Gly	Ile	Val	Met		
		180						185					190				
Met	Leu	Leu	Val	Gly	Trp	Met	Pro	Gly	Tyr	Leu	Phe	Phe	Asn	Ala	Thr		
	195					200						205					
Gly	Pro	Thr	Lys	Tyr	Ala	Gly	Leu	Ala	Lys	Ser	His	Phe	Asn	Pro	Tyr		
	210					215					220						
Ala	Ala	Phe	Phe	Leu	Pro	Lys	Glu	Arg	Leu	Ser	Ile	Trp	Trp	Ser	Asp		
225				230					235					240			
Leu	Cys	Phe	Leu	Ala	Ala	Leu	Tyr	Gly	Phe	Gly	Tyr	Gly	Val	Ser	Val		
				245					250					255			
Phe	Gly	Leu	Leu	Asp	Val	Ala	Arg	His	Tyr	Ile	Val	Pro	Tyr	Leu	Ile		
		260					265						270				
Cys	Asn	Ala	Tyr	Leu	Val	Leu	Ile	Thr	Tyr	Leu	Gln	His	Thr	Asp	Thr		
	275					280						285					
Tyr	Val	Pro	His	Phe	Arg	Gly	Asp	Glu	Trp	Asn	Trp	Leu	Arg	Gly	Ala		
	290					295					300						
Leu	Cys	Thr	Val	Asp	Arg	Ser	Phe	Gly	Ala	Trp	Ile	Asp	Ser	Ala	Ile		
305					310					315				320			
His	His	Ile	Ala	Asp	Thr	His	Val	Thr	His	His	Ile	Phe	Ser	Lys	Thr		
			325						330					335			
Pro	Phe	Tyr	His	Ala	Ile	Glu	Ala	Thr	Asp	Ala	Ile	Thr	Pro	Leu	Leu		
		340						345					350				
Gly	Lys	Tyr	Tyr	Leu	Ile	Asp	Pro	Thr	Pro	Ile	Pro	Leu	Ala	Leu	Trp		
	355					360						365					
Arg	Ser	Phe	Thr	His	Cys	Lys	Tyr	Val	Glu	Asp	Asp	Gly	Asn	Val	Val		
	370					375					380						
Phe	Tyr	Lys	Arg	Lys	Leu	Glu	Glu	Lys									
385					390												

<210> 44
 <211> 359
 <212> PRT

<213> Synechocystis sp.

<220>

<221> VARIANT

<222> (315)...(315)

<223> Xaa = Unknown or Other at position 315

<221> VARIANT

<222> (331)...(331)

<223> Xaa = Unknown or Other at position 331

<400> 44

Tyr	Phe	Phe	Leu	Asp	Val	Gly	Leu	Ile	Ala	Gly	Phe	Tyr	Ala	Leu	Ala
1				5					10					15	
Ala	Tyr	Leu	Asp	Ser	Trp	Phe	Phe	Tyr	Pro	Ile	Phe	Trp	Leu	Ile	Gln
			20					25					30		
Gly	Thr	Leu	Phe	Trp	Ser	Leu	Phe	Val	Val	Gly	His	Asp	Cys	Gly	His
		35					40					45			
Gly	Ser	Phe	Ser	Lys	Ser	Lys	Thr	Leu	Asn	Asn	Trp	Ile	Gly	His	Leu
	50					55					60				
Ser	His	Thr	Pro	Ile	Leu	Val	Pro	Tyr	His	Gly	Trp	Arg	Ile	Ser	His
65					70					75				80	
Arg	Thr	His	His	Ala	Asn	Thr	Gly	Asn	Ile	Asp	Thr	Asp	Glu	Ser	Trp
				85				90						95	
Tyr	Pro	Val	Ser	Glu	Gln	Lys	Tyr	Asn	Gln	Met	Ala	Trp	Tyr	Glu	Lys
			100					105					110		
Leu	Leu	Arg	Phe	Tyr	Leu	Pro	Leu	Ile	Ala	Tyr	Pro	Ile	Tyr	Leu	Phe
		115					120					125			
Arg	Arg	Ser	Pro	Asn	Arg	Gln	Gly	Ser	His	Phe	Met	Pro	Gly	Ser	Pro
	130					135					140				
Leu	Phe	Arg	Pro	Gly	Glu	Lys	Ala	Ala	Val	Leu	Thr	Ser	Thr	Phe	Ala
145					150					155					160
Leu	Ala	Ala	Phe	Val	Gly	Phe	Leu	Gly	Phe	Leu	Thr	Trp	Gln	Phe	Gly
			165					170						175	
Trp	Leu	Phe	Leu	Leu	Lys	Phe	Tyr	Val	Ala	Pro	Tyr	Leu	Val	Phe	Val
			180					185					190		
Val	Trp	Leu	Asp	Leu	Val	Thr	Phe	Leu	His	His	Thr	Glu	Asp	Asn	Ile
		195					200					205			
Pro	Trp	Tyr	Arg	Gly	Asp	Asp	Trp	Tyr	Phe	Leu	Lys	Gly	Ala	Leu	Ser
	210				215						220				
Thr	Ile	Asp	Arg	Asp	Tyr	Gly	Phe	Ile	Asn	Pro	Ile	His	His	Asp	Ile
225					230					235					240
Gly	Thr	His	Val	Ala	His	His	Ile	Phe	Ser	Asn	Met	Pro	His	Tyr	Lys
			245					250						255	
Leu	Arg	Arg	Ala	Thr	Glu	Ala	Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr
			260					265					270		
Arg	Tyr	Ser	Asp	Glu	Pro	Ile	Trp	Gln	Ala	Phe	Phe	Lys	Ser	Tyr	Trp
	275						280					285			
Ala	Cys	His	Phe	Val	Pro	Asn	Gln	Gly	Ser	Gly	Val	Tyr	Tyr	Gln	Ser
	290					295					300				
Pro	Ser	Asn	Gly	Gly	Tyr	Gln	Lys	Lys	Pro	Xaa	Leu	Ile	Leu	Ile	Glu
305					310					315					320
Ser	Asn	Gln	His	Arg	Glu	Gly	Arg	Gln	Tyr	Xaa	Met	Val	Leu	Leu	Pro
			325						330					335	
Ser	Asp	Arg	Leu	Met	Arg	Ser	Met	Glu	Glu	Val	Lys	Gln	Ser	His	Ser
			340					345					350		
Lys	Arg	Ser	Ala	Leu	Asn	Gln									
			355												

<210> 45

<211> 358
 <212> PRT
 <213> Saprolegnia diclina

<400> 45

Met	Thr	Glu	Asp	Lys	Thr	Lys	Val	Glu	Phe	Pro	Thr	Leu	Thr	Glu	Leu
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Lys	His	Ser	Ile	Pro	Asn	Ala	Cys	Phe	Glu	Ser	Asn	Leu	Gly	Leu	Ser
			20					25					30		
Leu	Tyr	Tyr	Thr	Ala	Arg	Ala	Ile	Phe	Asn	Ala	Ser	Ala	Ser	Ala	Ala
			35				40					45			
Leu	Leu	Tyr	Ala	Ala	Arg	Ser	Thr	Pro	Phe	Ile	Ala	Asp	Asn	Val	Leu
50						55					60				
Leu	His	Ala	Leu	Val	Cys	Ala	Thr	Tyr	Ile	Tyr	Val	Gln	Gly	Val	Ile
65					70					75					80
Phe	Trp	Gly	Phe	Phe	Thr	Val	Gly	His	Asp	Cys	Gly	His	Ser	Ala	Phe
				85					90					95	
Ser	Arg	Tyr	His	Ser	Val	Asn	Phe	Ile	Ile	Gly	Cys	Ile	Met	His	Ser
			100					105					110		
Ala	Ile	Leu	Thr	Pro	Phe	Glu	Ser	Trp	Arg	Val	Thr	His	Arg	His	His
			115				120					125			
His	Lys	Asn	Thr	Gly	Asn	Ile	Asp	Lys	Asp	Glu	Ile	Phe	Tyr	Pro	His
130						135					140				
Arg	Ser	Val	Lys	Asp	Leu	Gln	Asp	Val	Arg	Gln	Trp	Val	Tyr	Thr	Leu
145					150					155					160
Gly	Gly	Ala	Trp	Phe	Val	Tyr	Leu	Lys	Val	Gly	Tyr	Ala	Pro	Arg	Thr
				165					170					175	
Met	Ser	His	Phe	Asp	Pro	Trp	Asp	Pro	Leu	Leu	Leu	Arg	Arg	Ala	Ser
			180					185					190		
Ala	Val	Ile	Val	Ser	Leu	Gly	Val	Trp	Ala	Ala	Phe	Phe	Ala	Ala	Tyr
			195				200					205			
Ala	Tyr	Leu	Thr	Tyr	Ser	Leu	Gly	Phe	Ala	Val	Met	Gly	Leu	Tyr	Tyr
210						215					220				
Tyr	Ala	Pro	Leu	Phe	Val	Phe	Ala	Ser	Phe	Leu	Val	Ile	Thr	Thr	Phe
225					230					235					240
Leu	His	His	Asn	Asp	Glu	Ala	Thr	Pro	Trp	Tyr	Gly	Asp	Ser	Glu	Trp
				245					250					255	
Thr	Tyr	Val	Lys	Gly	Asn	Leu	Ser	Ser	Val	Asp	Arg	Ser	Tyr	Gly	Ala
			260					265					270		
Phe	Val	Asp	Asn	Leu	Ser	His	His	Ile	Gly	Thr	His	Gln	Val	His	His
			275				280					285			
Leu	Phe	Pro	Ile	Ile	Pro	His	Tyr	Lys	Leu	Asn	Glu	Ala	Thr	Lys	His
290						295					300				
Phe	Ala	Ala	Ala	Tyr	Pro	His	Leu	Val	Arg	Arg	Asn	Asp	Glu	Pro	Ile
305					310					315					320
Ile	Thr	Ala	Phe	Phe	Lys	Thr	Ala	His	Leu	Phe	Val	Asn	Tyr	Gly	Ala
				325					330					335	
Val	Pro	Glu	Thr	Ala	Gln	Ile	Phe	Thr	Leu	Lys	Glu	Ser	Ala	Ala	Ala
			340					345					350		
Ala	Lys	Ala	Lys	Ser	Asp										
			355												

<210> 46
 <211> 409
 <212> PRT
 <213> Caenorhabditis elegans

<220>
 <221> VARIANT
 <222> (389)...(389)

<223> Xaa = Unknown or Other at position 389

<400> 46

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Lys	Glu	Ala	Pro	Arg	Asp	Val	Asn	Ala	Asn	Thr	Lys	Gln	Ala	Thr	Thr
			20					25				30			
Glu	Glu	Pro	Arg	Ile	Gln	Leu	Pro	Thr	Val	Asp	Ala	Phe	Arg	Arg	Ala
		35				40					45				
Ile	Pro	Ala	His	Cys	Phe	Glu	Arg	Asp	Leu	Val	Lys	Ser	Ile	Arg	Tyr
	50					55					60				
Leu	Val	Gln	Asp	Phe	Ala	Ala	Leu	Thr	Ile	Leu	Tyr	Phe	Ala	Leu	Pro
65					70					75					80
Ala	Phe	Glu	Tyr	Phe	Gly	Leu	Phe	Gly	Tyr	Leu	Val	Trp	Asn	Ile	Phe
				85				90					95		
Met	Gly	Val	Phe	Gly	Phe	Ala	Leu	Phe	Val	Val	Gly	His	Asp	Cys	Leu
			100					105					110		
His	Gly	Ser	Phe	Ser	Asp	Asn	Gln	Asn	Leu	Asn	Asp	Phe	Ile	Gly	His
		115				120						125			
Ile	Ala	Phe	Ser	Pro	Leu	Phe	Ser	Pro	Tyr	Phe	Pro	Trp	Gln	Lys	Ser
	130					135					140				
His	Lys	Leu	His	His	Ala	Phe	Thr	Asn	His	Ile	Asp	Lys	Asp	His	Gly
145					150					155					160
His	Val	Trp	Ile	Gln	Asp	Lys	Asp	Trp	Glu	Ala	Met	Pro	Ser	Trp	Lys
				165					170					175	
Arg	Trp	Phe	Asn	Pro	Ile	Pro	Phe	Ser	Gly	Trp	Leu	Lys	Trp	Phe	Pro
			180					185					190		
Val	Tyr	Thr	Leu	Phe	Gly	Phe	Cys	Asp	Gly	Ser	His	Phe	Trp	Pro	Tyr
		195					200					205			
Ser	Ser	Leu	Phe	Val	Arg	Asn	Ser	Asp	Arg	Val	Gln	Cys	Val	Ile	Ser
	210					215					220				
Gly	Ile	Cys	Cys	Cys	Val	Cys	Ala	Tyr	Ile	Ala	Leu	Thr	Ile	Ala	Gly
225					230					235					240
Ser	Tyr	Ser	Asn	Trp	Phe	Trp	Tyr	Tyr	Trp	Val	Pro	Leu	Ser	Phe	Phe
				245					250					255	
Gly	Leu	Met	Leu	Val	Ile	Val	Thr	Tyr	Leu	Gln	His	Val	Asp	Asp	Val
			260					265					270		
Ala	Glu	Val	Tyr	Glu	Ala	Asp	Glu	Trp	Ser	Phe	Val	Arg	Gly	Gln	Thr
		275					280					285			
Gln	Thr	Ile	Asp	Arg	Tyr	Tyr	Gly	Leu	Gly	Leu	Asp	Thr	Thr	Met	His
	290					295					300				
His	Ile	Thr	Asp	Gly	His	Val	Ala	His	His	Phe	Phe	Asn	Lys	Ile	Pro
305					310					315					320
His	Tyr	His	Leu	Ile	Glu	Ala	Thr	Glu	Gly	Val	Lys	Lys	Val	Leu	Glu
				325					330					335	
Pro	Leu	Ser	Asp	Thr	Gln	Tyr	Gly	Tyr	Lys	Ser	Gln	Val	Asn	Tyr	Asp
			340					345					350		
Phe	Phe	Ala	Arg	Phe	Leu	Trp	Phe	Asn	Tyr	Lys	Leu	Asp	Tyr	Leu	Val
		355					360					365			
His	Lys	Thr	Ala	Gly	Ile	Met	Gln	Phe	Arg	Thr	Thr	Leu	Glu	Glu	Lys
	370					375					380				
Ala	Lys	Ala	Lys	Xaa	Lys	Asn	Ile	Pro	Cys	Arg	Ser	Arg	Val	Gln	Gln
385					390					395					400
Gln	Leu	Leu	Arg	Phe	His	Arg	Phe	Cys							
				405											

<210> 47

<211> 333

<212> PRT

<213> Saprolegnia diclina

<400> 47

Met	Cys	Lys	Gly	Gln	Ala	Pro	Ser	Lys	Ala	Asp	Val	Phe	His	Ala	Ala
1				5					10					15	
Gly	Tyr	Arg	Pro	Val	Ala	Gly	Thr	Pro	Glu	Pro	Leu	Pro	Leu	Glu	Pro
			20					25					30		
Pro	Thr	Ile	Thr	Leu	Lys	Asp	Leu	Arg	Ala	Ala	Ile	Pro	Ala	His	Cys
		35					40					45			
Phe	Glu	Arg	Ser	Ala	Ala	Thr	Ser	Phe	Tyr	His	Leu	Ala	Lys	Asn	Leu
	50					55					60				
Ala	Ile	Cys	Ala	Gly	Val	Phe	Ala	Val	Gly	Leu	Lys	Leu	Ala	Ala	Ala
65					70					75					80
Asp	Leu	Pro	Leu	Ala	Ala	Lys	Leu	Val	Ala	Trp	Pro	Ile	Tyr	Trp	Phe
				85					90					95	
Val	Gln	Gly	Thr	Tyr	Phe	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys
			100					105					110		
Gly	His	Gln	Ala	Phe	Ser	Ala	Ser	Glu	Ile	Leu	Asn	Asp	Thr	Val	Gly
		115					120					125			
Ile	Ile	Leu	His	Ser	Leu	Leu	Phe	Val	Pro	Tyr	His	Ser	Trp	Lys	Ile
	130					135					140				
Thr	His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser	Cys	Glu	Asn	Asp	Glu
145					150					155					160
Val	Phe	Thr	Pro	Thr	Pro	Arg	Ser	Val	Val	Glu	Ala	Lys	His	Asp	His
				165					170					175	
Ser	Leu	Leu	Glu	Glu	Ser	Pro	Leu	Tyr	Asn	Leu	Tyr	Gly	Ile	Val	Met
			180					185					190		
Met	Leu	Leu	Val	Gly	Trp	Met	Pro	Gly	Tyr	Leu	Phe	Phe	Asn	Ala	Thr
		195					200					205			
Gly	Pro	Thr	Lys	Tyr	Ala	Gly	Leu	Ala	Lys	Ser	His	Phe	Asn	Pro	Tyr
	210					215					220				
Ala	Ala	Phe	Phe	Leu	Pro	Lys	Glu	Arg	Leu	Ser	Ile	Trp	Trp	Ser	Asp
225					230					235					240
Leu	Cys	Phe	Leu	Ala	Ala	Leu	Tyr	Gly	Phe	Gly	Tyr	Gly	Val	Ser	Val
				245					250					255	
Phe	Gly	Leu	Leu	Asp	Val	Ala	Arg	His	Tyr	Ile	Val	Pro	Tyr	Leu	Ile
			260					265					270		
Cys	Asn	Ala	Tyr	Leu	Val	Leu	Ile	Thr	Tyr	Leu	Gln	His	Thr	Asp	Thr
		275					280					285			
Thr	Pro	Leu	Leu	Gly	Lys	Tyr	Tyr	Leu	Ile	Asp	Pro	Thr	Pro	Ile	Pro
	290					295					300				
Leu	Ala	Leu	Trp	Arg	Ser	Phe	Thr	His	Cys	Lys	Tyr	Val	Glu	Asp	Asp
305					310					315					320
Gly	Asn	Val	Val	Phe	Tyr	Lys	Arg	Lys	Leu	Glu	Glu	Lys			
				325					330						

<210> 48

<211> 412

<212> PRT

<213> *Gossypium hirsutum*

<220>

<221> VARIANT

<222> (9)...(9)

<223> Xaa = Unknown or Other at position 9

<221> VARIANT

<222> (403)...(403)

<223> Xaa = Unknown or Other at position 403

<400> 48

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Leu Arg Val Ser Ser Thr Trp Arg Xaa Thr Ala Phe Phe Lys Ala Ser
1      5      10      15
Lys Met Gly Ala Gly Gly Arg Met Pro Ile Asp Gly Ile Lys Glu Glu
20      25      30
Asn Arg Gly Ser Val Asn Arg Val Pro Ile Glu Lys Pro Pro Phe Thr
35      40      45
Leu Gly Gln Ile Lys Gln Ala Ile Pro Pro His Cys Phe Arg Arg Ser
50      55      60
Leu Leu Arg Ser Phe Ser Tyr Val Val His Asp Leu Cys Leu Ala Ser
65      70      75      80
Phe Phe Tyr Tyr Ile Ala Thr Ser Tyr Phe His Phe Leu Pro Gln Pro
85      90      95
Phe Ser Tyr Ile Ala Trp Pro Val Tyr Trp Val Leu Gln Gly Cys Ile
100     105     110
Leu Thr Gly Val Trp Val Ile Ala His Glu Trp Gly His His Ala Phe
115     120     125
Arg Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu Ile Leu His Ser
130     135     140
Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His
145     150     155     160
His Ser Asn Thr Gly Ser Met Glu Arg Asp Glu Val Phe Val Pro Lys
165     170     175
Pro Lys Ser Lys Leu Ser Cys Phe Ala Lys Tyr Leu Asn Asn Pro Pro
180     185     190
Gly Arg Val Leu Ser Leu Val Val Thr Leu Thr Leu Gly Trp Pro Met
195     200     205
Tyr Leu Ala Phe Asn Val Ser Gly Arg Tyr Tyr Asp Arg Leu Ala Ser
210     215     220
His Tyr Asn Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
225     230     235     240
Val Tyr Ile Ser Asp Thr Gly Ile Phe Ala Val Ile Tyr Val Leu Tyr
245     250     255
Lys Ile Ala Ala Thr Lys Gly Leu Ala Trp Leu Leu Cys Thr Tyr Gly
260     265     270
Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
275     280     285
Gln His Thr His Ser Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
290     295     300
Trp Leu Arg Gly Ala Leu Ser Thr Met Asp Arg Asp Phe Gly Val Leu
305     310     315     320
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
325     330     335
Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
340     345     350
Lys Pro Ile Leu Gly Lys Tyr Tyr Pro Phe Asp Gly Thr Pro Ile Tyr
355     360     365
Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp
370     375     380
Val Gly Gly Gly Gly Gly Ser Lys Gly Val Phe Trp Tyr Arg Asn
385     390     395     400
Lys Phe Xaa Arg Pro Thr Asn Cys Leu Ile Ala Gly
405     410

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<210> 49

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 1 from Example 3

<400> 49

Thr	Arg	Ala	Ala	Ile	Pro	Lys	His	Cys	Trp	Val	Lys
1				5					10		

<210> 50

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 2 from Example 3

<400> 50

Ala	Leu	Phe	Val	Leu	Gly	His	Asp	Cys	Gly	His	Gly	Ser	Phe	Ser
1				5					10				15	

<210> 51

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 3 from Example 3

<400> 51

Pro	Tyr	His	Gly	Trp	Arg	Ile	Ser	His	Arg	Thr	His	His	Gln	Asn
1				5					10				15	

<210> 52

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 4 from Example 3

<221> VARIANT

<222> (5)...(5)

<223> Xaa = D or H at position 5

<221> VARIANT

<222> (7)...(7)

<223> Xaa = D or Y at position 7

<400> 52

Gly	Ser	His	Phe	Xaa	Pro	Xaa	Ser	Asp	Leu	Phe	Val
1				5					10		

<210> 53

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 5 from Example 3

<221> VARIANT

<222> (3)...(3)

<223> Xaa = Y or F at position 3

<221> VARIANT

<222> (4)...(4)

<223> Xaa = L or V at position 4

<221> VARIANT

<222> (11)...(11)

<223> Xaa = L or I at position 11

<400> 53

Trp	Ser	Xaa	Xaa	Arg	Gly	Gly	Leu	Thr	Thr	Xaa	Asp	Arg
1				5					10			

<210> 54

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 6 from Example 3

<400> 54

His	His	Asp	Ile	Gly	Thr	His	Val	Ile	His	His	Leu	Phe	Pro	Gln
1				5				10					15	

<210> 55

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 7 from Example 3

<221> VARIANT

<222> (2)...(2)

<223> Xaa = L or F at position 2

<221> VARIANT

<222> (5)...(5)

<223> Xaa = Q or K at position 5

<221> VARIANT

<222> (12)...(12)

<223> Xaa = V or I at position 12

<400> 55

His	Xaa	Phe	Pro	Xaa	Ile	Pro	His	Tyr	His	Leu	Xaa	Glu	Ala	Thr
1				5				10				15		

<210> 56

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 8 from Example 3

<221> VARIANT

<222> (3)...(3)

<223> Xaa = A or I at position 3

<221> VARIANT

<222> (6)...(6)

<223> Xaa = L or F at position 6

<400> 56

His	Val	Xaa	His	His	Xaa	Phe	Pro	Gln	Ile	Pro	His	Tyr	His	Leu
1				5					10					15

<210> 57

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 1 from Example 7

<221> VARIANT

<222> (2)...(2)

<223> Xaa = N or E at position 2

<221> VARIANT

<222> (10)...(10)

<223> Xaa = D or E at position 10

<221> VARIANT

<222> (11)...(11)

<223> Xaa = A or C at position 11

<400> 57

Pro	Xaa	Phe	Thr	Ile	Lys	Glu	Ile	Arg	Xaa	Xaa	Ile	Pro	Ala	His	Cys
1				5					10					15	
Phe															

<210> 58

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 2 from Example 7

<221> VARIANT

<222> (3)...(3)

<223> Xaa = H or F at position 3

<221> VARIANT

<222> (11)...(11)

<223> Xaa = V or Y at position 11

<221> VARIANT

<222> (13)...(13)

<223> Xaa = I or L at position 13

<221> VARIANT

<222> (16)...(16)

<223> Xaa = A or L at position 16

<400> 58

Met Pro Xaa Tyr His Ala Glu Glu Ala Thr Xaa His Xaa Lys Lys Xaa
 1 5 10 15

<210> 59

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 3 from Example 7

<221> VARIANT

<222> (2)...(2)

<223> Xaa = L or V at position 2

<221> VARIANT

<222> (5)...(5)

<223> Xaa = A or I at position 5

<221> VARIANT

<222> (6)...(6)

<223> Xaa = C or M or A at position 6

<221> VARIANT

<222> (9)...(9)

<223> Xaa = V or I at position 9

<221> VARIANT

<222> (11)...(11)

<223> Xaa = L or G or C at position 11

<400> 59

Pro Xaa Tyr Trp Xaa Xaa Gln Gly Xaa Val Xaa Thr Gly Val Trp
 1 5 10 15

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein Motif 4 from Example 7

<221> VARIANT

<222> (6)...(6)

<223> Xaa = L or F at position 6

<221> VARIANT

<222> (9)...(9)

<223> Xaa = T or Q at position 9

<400> 60

His Val Ala His His Xaa Phe Ser Xaa Met Pro His Tyr His Ala
 1 5 10 15